SEQUENCE LISTING

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<120> TNF-alpha Binding Molecules

<130> X-16758M

<140> PCT/US04/00290
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<151> 2003-01-08

<160> 122

<170> PatentIn version 3.3

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1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp His Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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gatcagtctc caaagctcct catcaagtat gcttctgagt ctatgtctgg ggtcccctcg 180

aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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ccagggaagg ggctggagtg ggttggcgaa attagatcaa aatctattaa ttctgcaaca 180

cattatgcgg agtctgtgaa agggagattc accatctcaa gagatgattc aaagaactca 240

ctgtacctgc agatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga 300

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1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Tyr Ser
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp His Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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gatcagtctc caaagctcct catcaagtat gcttctgagt ctaggtctgg ggtcccctcg 180

aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240

gaagatgctg ccacgtatta ctgtcaacaa agtcatagct ggcatttcac gttcggccaa 300

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Ser Asn His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
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ccagggaagg ggctggagtg ggttggcgaa attagatcaa aatctatgaa ttctgcaaca 180

cattatgcgg agtctgtgaa agggagattc accatctcaa gagatgattc aaagaactca 240

ctgtacctgc agatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga 300

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Arg Ala Ser Gln Phe Val Gly Leu Ser Ile His
1 5 10

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Arg Ala Ser Gln Phe Val Gly Met Ser Ile His

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Arg Ala Ser Gln Phe Val Gly Tyr Ser Ile His
1 5 10

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<400> 19

Tyr Ala Ser Glu Ser Met Ser
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<400> 21

Tyr Ala Ser Glu Tyr Met Ser
1 5

<210> 22
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<400> 22
tatgcttctg agtatatgtc t 21

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<400> 25

Tyr Ala Ser Glu Ser Arg Ser
1 5

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<400> 26
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Tyr Ala Ser Glu Ser Lys Ser
1 5

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Tyr Ala Ser Glu Xaa Xaa Ser
1 5

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<400> 33

Gln Gln Ser His Ser Trp His Phe Thr
1 5

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caacaaagtc atagctggca tttcacg 27

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<400> 35

Gly Phe Thr Phe Ser Asn His Trp Met Asn
1 5 10

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Gly Phe Lys Phe Ser Asn His Trp Met Asn
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Gly Phe Pro Phe Ser Asn His Trp Met Asn
1 5 10

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Val Lys Gly

<210> 44
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<212> DNA
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<210> 45
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<400> 45

Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 46
<211> 57
<212> DNA
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<220>
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gaaattagat caaaatctat gaattctgca acacattatg cggagtctgt gaaaggg 57

<210> 47
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Val Lys Gly

<210> 48
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<400> 49

Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Arg Ser
1 5 10 15

Val Lys Gly

<210> 50
<211> 57
<212> DNA
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<210> 51
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1 5 10 15

Val Lys Gly

<210> 52
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<400> 53

Asn Tyr Tyr Gly Ser Thr Tyr Asp His
1 5

<210> 54
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aattactacg gtagtaccta cgaccat 27

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<400> 55

Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Arg Ser
1 5 10 15

Val Lys Gly

<210> 56
<211> 57
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<210> 57

<211> 23
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Glu Lys Val Thr Ile Thr Cys
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Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile Lys
1 5 10 15

<210> 59
<211> 32
<212> PRT
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<400> 59

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
20 25 30

<210> 60
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<400> 60

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 61
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atcacctgc 69

<210> 62
<211> 45
<212> DNA
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tggtaccagc agaagccaga tcagtctcca aagctcctca tcaag 45

<210> 63
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<212> DNA
<213> Homo sapiens

<400> 63
ggggtcccct cgaggttcag tggcagtgga tctgggacag atttcaccct caccatcaat 60

agcctggaag ctgaagatgc tgccacgtat tactgt 96

<210> 64
<211> 30
<212> DNA
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<400> 64
ttcggccaag ggaccaaggt ggaaatcaaa 30

<210> 65
<211> 25
<212> PRT
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<400> 65

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 66
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<400> 66

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
1 5 10

<210> 67
<211> 32
<212> PRT
<213> Homo sapiens

<400> 67

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

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<211> 11

<212> PRT
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<400> 68

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 69
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<212> DNA
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tcctgtgcag cctct 75

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<211> 42
<212> DNA
<213> Homo sapiens

<400> 70
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<210> 71
<211> 96
<212> DNA
<213> Homo sapiens

<400> 71
agattcacca tctcaagaga tgattcaaag aactcactgt acctgcagat gaacagcctg 60

aaaaccgagg acacggccgt gtattactgt gctaga 96

<210> 72
<211> 33
<212> DNA
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<400> 72
tggggccaag ggaccctggt caccgtctcc tca 33

<210> 73
<211> 11
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<400> 73

Arg Ala Pro Gln Phe Val Gly Ser Ser Ile His
1 5 10

<210> 74
<211> 33
<212> DNA
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<400> 74
agggcccctc agttcgttgg ctcaagcatc cac 33

<210> 75
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<223> The residue in this position could be any amino acid

<400> 75

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1 5 10

<210> 76
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<222> (7)..(9)
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<210> 77
<211> 11
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<220>
<223> Synthetic Construct

<400> 77

Arg Ala Ser Gln Phe Val Tyr Ser Ser Ile His
1 5 10

<210> 78
<211> 33
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<400> 78
agggccagtc agttcgttta ttcaagcatc cac 33

<210> 79
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Arg Ala Ser Gln Phe Val Xaa Ser Ser Ile His
1 5 10

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<220>
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<211> 9
<212> PRT
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<400> 81

Gln Gln Ser His Trp Trp His Phe Thr
1 5

<210> 82
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<400> 82
caacaaagtc attggtggca tttcacg 27

<210> 83
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<400> 83

Gln Gln Ser His Xaa Trp His Phe Thr
1 5

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caacaaagtc atnnntggca tttcacg 27

<210> 85
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<212> DNA
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gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 120

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 180

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 240

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagcagag 300

cccaaatctt ctactagtgt tctctaccca tatgatgtac ctgattatgc atcatag 357

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tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180

agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 300

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<400> 87

Gly Phe Thr Phe Arg Asn His Trp Met Asn
1 5 10

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Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr Phe Tyr Ala Glu Ser
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Val Lys Gly

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<400> 91

Asn Tyr Tyr Gly Ser Tyr Tyr Asp His
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aattactacg gtagttatta cgaccat 27

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<400> 93

Val Thr Thr Gln Phe Val Gly Tyr Ala Ile His
1 5 10

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Tyr Ala Ser Ser Ser Arg Ser
1 5

<210> 96

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Gln Gln Ser His Gly Trp Pro Phe Thr
1 5

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caacaaagtc atgggtggcc tttcacg 27

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Gly Phe Lys Phe Arg Asn His Trp Met Asn
1 5 10

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Gly Phe Asp Phe Arg Asn His Trp Met Asn
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<400> 103

Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr Phe Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

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Ala Ala Ser Gln Phe Val Gly Gln Ala Ile His
1 5 10

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Tyr Ala Asn Glu Ser Arg Ser
1 5

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<400> 115

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr Phe Tyr Ala Glu
50 55 60

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Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Tyr Tyr Asp His Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
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Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
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Asp Arg Val Thr Ile Thr Cys Val Thr Thr Gln Phe Val Gly Tyr Ala
            20                  25                  30

Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Tyr Ala Ser Ser Ser Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser His Gly Trp Pro Phe
                85                  90                  95
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205

Asn Arg Gly Glu Cys
    210
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<400> 118
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<210> 119
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<400> 119
gacagatggt gcagccacag t 21

<210> 120
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ctctccacag gtgtccactc ccaggtccaa ctgcaggtc 39

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<220>
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ctctccacag gtgtccactc c 21

<210> 122
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<400> 122
gaagaccgat gggcccttgg t 21